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F. # 2014R01047

UNITED STATES DISTRICT COURT
EASTERN DISTRICT OF NEW YORK

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UNITED STATES OF AMERICA

- against - Docket No. 14–CR-414 (BMC)

RASHAWN JERMAINE SMALLS,

Defendant.

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AFFIDAVIT OF CRAIG O'CONNOR

I, DR. CRAIG O'CONNOR, pursuant to 28 U.S.C. § 1746, declare as follows:

1. I am a Criminalist IV and Assistant Technical Leader for Nuclear DNA Operations in the Department of Forensic Biology at the New York City Office of Chief Medical Examiner ("OCME") and a Clinical Assistant Professor in the Department of Forensic Medicine at New York University Medical Center.

2. I have a Bachelor's of Science in physiology and neurobiology from the University of Connecticut. Prior to attending graduate school, I spent a year and a half as a research technician at the Yale University School of Medicine performing biochemical assays dealing with uterine and prostate cancer. In 2007, I received a Master's of Science and in 2008 a Ph.D both in genetics and genomics from the University of Connecticut. During graduate school, my research focused on forensic human identification. In 2008, I began working at the OCME.

3. As an OCME Criminalist, my main duties include the day-to-day examination of evidence from crimes such as homicides, assaults, sexual assaults, property crimes and cold cases, DNA analysis, writing reports and testifying in court.

4. DNA, or deoxyribonucleic acid, is the inherited genetic material found in human cells, which contains markers that differ from person to person. DNA within a cell is tightly packaged in structures known as chromosomes. While DNA spends much of its time in chromosome form, during cell division, DNA uncoils so that it can be copied. When unraveled, DNA's structure most represents a twisted ladder, or "double helix." The rungs of this ladder are made of the following four bases: adenine, thymine, guanine, and cytosine. Adenine bonds with thymine, while guanine bonds with cytosine and those units form what is known as base pairs. The sequence in which these bases bond determines the biological instructions a particular strand of DNA contains. While approximately 99% of human DNA material is identical, no two people have the same DNA sequence.

5. Forensic DNA profiling targets areas of DNA that vary from person to person. DNA testing can determine these genetic markers and compare biological samples from different individuals. Polymerase Chain Reaction or "PCR" is a scientific process during which DNA material is duplicated many times, allowing very small samples of DNA to be accurately tested. Short Tandem Repeats or "STR"s are the specific group of loci (locus in the singular) that are used to type and compare DNA. These are short segments of DNA that are repeated a number of times in tandem, or in a row.

6. Using PCR/STR, an analyst looks at the length variation at an STR locus, i.e., how many times a particular set of bases repeats at that STR location. The number of repeats at a particular location constitutes the DNA type or "allele" present at that

location. For example, if ten repeats of a sequence of bases were present in the STR locus, the DNA allele would be marked "10." Since a human being receives half of his DNA from one biological parent and half of his DNA from the other biological parent, each person has two DNA alleles at each locus. Thus, the DNA type at one locus may be "10, 11." This "allele call" shows that ten repeats of one STR unit came from one parent, and eleven repeats of the same STR unit came from the other parent. A locus with two different numbers is "heterozygous." If only one number appears at a particular locus, it means the person inherited the same number of repeats from each parent, and the locus is "homozygous."

7. DNA testing involves four basic steps: (1) extraction, (2) quantitation, (3) PCR amplification, and (4) analysis of the resulting DNA alleles. See Exhibit A (Laboratory Report by the OCME, dated June 4, 2014 (hereinafter "June 4 Report")). Extraction is the recovery of DNA from biological samples such as blood, bone, hair, saliva, semen, and skin cells. Quantitation is the measurement of the amount of DNA extracted from the relevant samples. If sufficient DNA is detected, amplification and analysis can be attempted. Amplification produces larger amounts of DNA from small starting amounts of DNA by repeated cycles of copying. After amplification, the alleles present in the DNA sample are analyzed and identified.

8. OCME was established in 1918. It identifies the manner and cause of death in specified cases and provides state of the art forensic analysis. OCME was the first governmental agency of its kind in the United States, and established the first toxicology laboratory in 1918 and the first serology laboratory in 1938. DNA analysis at OCME is done by the Department of Forensic Biology. The OCME Forensic Biology Laboratory has been performing DNA testing in criminal cases since 1991. OCME's DNA analysis includes the

examination of homicide, sexual assault, and other crime evidence for DNA extraction and typing, and that analysis may either incriminate or exclude a suspect. OCME performs more DNA analyses than any other public laboratory in the country. See Exhibit B (Press Release, New York City Office of the Mayor, Mayor Bloomberg and Chief Medical Examiner Hirsh Cut Ribbon at Largest Government DNA Laboratory in the Country (July 18, 2007)).

9. The OCME is subject to federal and state regulations. The FBI's quality assurance standards require OCME, and any other public forensic laboratory that is authorized to upload DNA profiles to the FBI-operated Combined DNA Index System ("CODIS"), to be accredited. State accreditation is granted by the New York State Forensic Science Commission with a binding recommendation from its DNA Subcommittee. New York State legislation designated the American Society of Crime Lab Directors/Laboratory Accreditation Board ("ASCLD/LAB") as the accrediting body for forensic labs in this state. See Exhibit C (OCME ASCLD Accreditation Certificate). Accreditation requires a full assessment by a team of qualified DNA scientist assessors every five years, annual surveillance visits by ASCLD/LAB staff auditors, an inspection report, and an annual accreditation review report. In addition, biannual external audits are conducted by expert entities such as the National Forensic Science and Technology Center ("NFSTC"). NFSTC lead members are DNA auditors trained by the Federal Bureau of Investigation ("FBI"). The assessors use International Standards (ISO 17025) and US Federal Standards (FBI DNA Quality Assurance Standards) to evaluate facilities and equipment, training, whether or not the laboratory is following standard operating procedures, validations for new equipment and techniques, and casework reports. In the alternate years, OCME performs an internal audit and reports the results to the FBI and ASCLD/LAB.

10. When there are 100 picograms or more of DNA present in a sample, OCME performs High Copy Number ("HCN") DNA analysis.[1] See Exhibit D (Adele A. Mitchell, et al., Validation of a DNA Mixture Statistics Tool Incorporating Allelic Drop-Out and Drop-In, FORENSIC SCI INT'L GENET. 2012 Dec; 6(6):749-61). OCME uses the Applied Biosystems AmpFISTR Identifiler® PCR Amplification Kit (the "Identifiler Kit") with 28 amplification cycles for HCN DNA testing. The User's Guide for the Identifiler Kit notes that the Identifiler Kit has been tested at 27, 28, 29, 30, and 31 cycles, and "none of the cycle numbers tested produced nonspecific peaks," i.e., none of the cycles produced that stochastic or random effect. Exhibit E (Identifiler Kit User's Guide) at 68. Nonetheless, the User's Guide indicates that while the kit has been tested at certain quantities, and under certain conditions, it is important for individual laboratories to conduct their own individual validation studies. See, e.g., Exhibit E at 66 ("[The manufacturer's] experiments, while not exhaustive, are appropriate for a manufacturer, in our opinion. Each laboratory using the Identifiler Kit should perform appropriate validation studies."), and at 22 ("it is recommended that each laboratory determine the optimum cycle number based on internal validation studies.").

11. The forensic statistical tool ("FST") is a tool to help scientists interpret DNA mixtures found on evidence. In a single source sample, that is, a sample coming from only one contributor, it is clear that the two alleles at each locus belong to one person, and it is easy to determine the profile. For example, if a bloodstain is found on a T shirt, and that bloodstain comes from one person (single source), a calculation called the "random match

[1] There is approximately 6 picograms of DNA in a single cell. Where there is less than 100 picograms of DNA present in a sample, OCME may perform Low Copy Number ("LCN") DNA testing, also known as High Sensitivity Testing.

probability" or RMP, is done. This provides a statistic such as "one in greater than a trillion", expressed as follows: the chances of seeing this profile randomly in the general population are one in greater than a trillion people. In fact, although it is simple to calculate the RMP with a single source profile, that number can also be expressed as a likelihood ratio: the profile found on the evidence is one trillion times more likely if it came from the defendant than if it came from a different, unrelated person (and not the defendant).

12. While it is relatively easy to assign a statistical weight to single source samples, mixtures present more difficult challenges. This is because in a mixture, one may see more than two alleles, or pieces of DNA, at each locus.

13. Mixture interpretation requires scientists to determine which alleles at a locus belong to one person and which belong to another. The minimum number of people contributing to the mixture can be determined by counting the number of alleles at each locus. For example, if there are three or four alleles at a particular locus, at least two people are present; if there are five alleles, at least three people are present. Sometimes, when the mixtures are so uneven, and one person is present in far greater proportions than the other, it is possible to "deconvolute" or separate out the people in the mixture. In those cases, you can determine the major donor by looking at the peak heights representing pieces of DNA on the electropherogram, the printout generated by the DNA testing instrument called the Capillary Electrophoresis machine whose printout resembles an EKG. It is then possible to treat a major donor like a single source profile and use the RMP and get a "one in greater than a trillion" type statistic. However, when the mixtures are too evenly balanced to separate out the various components, scientists say a mixture is "suitable for comparison". That means one can look at a DNA profile generated from a suspect or victim exemplar and

see whether the alleles present in the exemplar are also present in the evidence mixture. In that way one can see whether the person could be a contributor to, or included in the evidence mixture.

14. Up until the development of the FST, scientists at OCME had a limited number of ways to describe associations between evidence and individuals. If the evidence was a single source sample or a major donor treated like a single source sample, an RMP could be calculated. In an irresolvable mixture suitable only for comparison, OCME analysts could see whether all of the suspect's alleles were present in the mixture. There are several qualitative conclusions that can be made upon comparing a person's profile to a mixture. If most of their alleles are missing from the mixture, then they are excluded as a possible contributor. If all of their alleles are present in the mixture then they can be included as a possible contributor. If most but not all of their alleles are present in the mixture and the absence of the alleles can be scientifically explained by possible "allelic drop-out" (as described below) or other means, then the person cannot be excluded as a possible contributor to the mixture. In general, forensic statistics are not calculated for exclusions. If and only if all the suspect's alleles were present, the OCME would calculate a statistic called the combined probability of inclusion ("CPI").

15. An overwhelming consensus developed in the scientific community that a statistic must be applied to any positive association between a suspect and evidence. The Scientific Working Group for DNA Analysis Methods ("SWGDAM") is the body now responsible for making recommendations to the forensic DNA community in the United States. SWGDAM, comprised of scientists from international, federal, state and local forensic labs, serves as a forum to discuss and evaluate forensic biology methods, protocols,

training and research to enhance forensic testing as well as to provide recommendations to the FBI Director on quality assurance standards for forensic DNA analysis. The 2010 SWGDAM Interpretation Guideline 4.1 states that the laboratory must perform statistical analysis in support of any inclusion that is determined to be relevant in the context of a case, irrespective of the number of alleles detected and the quantitative value of the statistical analysis. The National Academy of Sciences recommended in its 2009 report, Strengthening Forensic Sciences in the United States: A Way Forward, that a statistical weight must be applied to all positive associations. In addition, the DNA Commission of the International Society of Forensic Genetics has recommended that a likelihood ratio be applied to mixture interpretations.

16. In order to comply with the best scientific practices, the OCME developed the FST to give a quantitative, that is, a statistical, as well as a qualitative, way to describe the strength of probative evidence in a criminal case. The FST is computer software developed by the OCME Forensic Biology lab to calculate "likelihood ratios" or "LRs." LRs are statistics relating to the likelihood of one scenario over another. The first scenario is the probability of seeing a mixture of DNA found on evidence in a case if a suspect did contribute to the mixture. The second scenario is the probability of seeing a mixture of DNA on the evidence if the defendant did not contribute to the mixture but rather, unknown persons did. It is not a statement that the suspect's profile is part of the DNA mixture present on evidence. OCME offers the following qualitative interpretation of LR: if the LR is 1.0 to 10, then the evidence provides limited support. If the LR is 10 to 100, that provides moderate support. If the LR is 100 to 1000, it provides strong support, and if the LR is greater than 1000, the evidence provides very strong support of one scenario over the other.

A LR of exactly 1.0 is considered to be inconclusive or no conclusions be drawn as to which scenario has more support.

17. The software used in FST applies to forensic DNA analysis mathematical and statistical principles that have been established and used in other fields for decades. FST was developed over the course of two years by a team of experts at the OCME holding graduate degrees in human genetics and biomolecular chemistry, among other things, and was subjected to rigorous testing and peer review. The curricula vitae for the FST development team are attached as Exhibit F. The statistical analysis underlying the likelihood ratio used by FST derives from principles first developed more than two centuries ago by Thomas Bayes, an 18th-Century English mathematician. Those principles, part of a system known as "Bayesian analysis" have long been applied, and are well-established, in other scientific fields, including medicine and genetics.[2] They are used in paternity testing and were used to identify remains recovered following the September 11, 2001 attack on the World Trade Center.[3]

18. FST has been approved by the DNA Subcommittee of the New York State Commission on Forensic Science, a group of highly regarded scientists and experts in

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[2] See, e.g., Deborah Ashby, "Bayesian Statistics in Medicine: A 25 Year Review," 25 Statistics in Medicine 3589-3631 (2006) ("[I]t seems there is now no area of medical statistics untouched by Bayesian approaches."); Matthew Stephens and David J. Balding, "Bayesian Statistical Methods for Genetic Association Studies," 10 Nature Reviews Genetics 681 690 (2009).

[3] See Leslie G. Biesecker, et al., "DNA Identifications After the 9/11 World Trade Center Attack," 30 Science 1122-23 (November 15, 2005) (Likelihood ratio used in kinship analysis following 9/11 attack "compares the probabilities of observing a given DNA profile if a victim sample belonged to a particular missing individual (based on the stated genetic relationship of kin providing reference samples) to the chance of observing the profile if it was from an unrelated person.")

the field of DNA analysis who advise the Commission on Forensic Science on matters relating to implementation of scientific controls and quality assurance procedures for the performance of forensic DNA analysis. The DNA Subcommittee evaluates all methodologies that New York laboratories propose to use for forensic DNA analysis. See id. at (13(b)). See N.Y. Executive Law Article 49-B ' 995-B (they are charged with "increas[ing] and maintain[ing] the effectiveness, efficiency, reliability, and accuracy of forensic laboratories, including forensic DNA laboratories," and "ensur[ing] that forensic analyses, including forensic DNA testing, are performed in accordance with the highest scientific standards practicable."). Its members include distinguished experts in the fields of forensic science, population genetics, molecular biology and laboratory standards. The Subcommittee makes binding recommendations to the Commission on Forensic Science, which, under Article 49-B, holds ultimate authority for accrediting forensic laboratories throughout the state. Among the Commission's 14 members are directors of public forensic labs, District Attorneys, three members of the defense bar (including Barry Scheck and Peter Neufeld of the Innocence Project) and retired judges.

19. OCME first presented the analytic method underlying FST to the DNA Subcommittee of the New York State Commission on Forensic Science in November 2009. Following its initial presentation to the DNA Subcommittee and comments made by the subcommittee members, OCME spent several months testing and validating the results generated by FST. Among other things, OCME tested the parameters used by FST regarding what are known as "drop-in" and "drop-out" rates, which are used in calculating an LR.

20. Drop-out occurs when an allele that is actually known to exist at a particular locus in a DNA sample is not found in the analysis. Drop out occurs for several

reasons. The first is a function of the amount of DNA being tested. When a very small amount of DNA is tested, the amplification portion of the testing may not pick up all of the pieces of DNA in the profile, and the testing will reflect only those pieces that were picked up. Those pieces not picked up are said to have "dropped out" because even though they are part of the original sample, they will not be amplified, or copied, and will therefore not be represented in the result.[4] A second reason drop out may occur is when a sample is degraded. DNA varies by amplicon size, and longer pieces of DNA will break down faster than shorter pieces. That means some longer pieces of DNA may not be detected, and will have "dropped out" of the results. A third reason for drop out involves the relative proportions of a mixture. If the mixture is not even, and if one person is represented in greater amounts, more pieces of one donor's DNA might be grabbed during sampling and therefore some DNA would not be detected. Finally, inhibition might occur. Something in a sample, such as indigo dye in a pair of denim jeans, might interfere with the testing process and inhibit amplification of some pieces of DNA. Drop-in occurs when an allele is detected during analysis that is known not to belong to the person or persons contributing to the sample. Drop-in is often attributable to contamination of the sample or the testing equipment or from a very minor contributor's DNA that may have been on the item.

21. To develop the drop-in/drop-out parameters used in FST, OCME conducted an empirical validation study on 2,041 DNA samples, drawn from known contributors, of varying weights and mixtures, and used that data to deduce probabilities of

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[4] For instance, if four marbles were chosen randomly from a sample consisting of 12 black marbles and 12 white marbles, four black marbles might be grabbed from the sample and tested, missing the white marbles. The white marbles would have "dropped-out" even though they were part of the original sample.

drop-in and drop-out in a given DNA sample. During this time consuming phase, OCME actually counted how often a piece of DNA drop-out occurred and determined that it correlated with the quantity of DNA, among other factors. Thereafter, they compared the individual profiles of the known contributors to mixtures of DNA derived from two, three, or four persons. The mixtures contained various amounts of DNA from each contributor which varied from 25 picograms near the bottom level of the low template range, to 500 picograms near the upper level of the high template range. The mixture ratios included 1:1 and 4:1 for two-person DNA mixtures and 1:1:1 and 5:1:1 for three-person mixtures. Studies were performed which established the probability that DNA would drop out at particular loci. Drop-in rates also were ascertained. These drop-out and drop-in rates were then subjected to extensive testing both by computer and manual calculation to validate them.

22. The FST determines a drop-out rate based on the quantity of DNA amplified, the number of amplification cycles, the number of contributors to the sample, and the approximate mixture ratio (either unequal or approximately equal).

23. In March 2010, OCME presented the results of its drop-in/drop-out data to the Subcommittee, as well as a plan to validate that data.

24. In executing the validation plan, FST was subjected to a further extensive and detailed validation process resulting in the accumulation of data filling 45 large binders. More than 400 mock DNA casework samples consisting of saliva, blood, and touched items were created using materials provided by the known contributors. The donors for these mock casework samples were 85 people who represented a wide range of racial and ethnic backgrounds found in the city of New York. The donors included volunteers from the lab itself as well as autopsy samples. Different combinations of those 85 donors created 439

touched and purposeful mixtures. These mixtures were used for 480 test runs through the electrophoresis instrument—272 two-person mixtures consisting of 160 low template DNA samples and 112 high template DNA samples and 208 three-person mixtures, consisting of 97 low template DNA samples and 111 high-template DNA samples.[5] DNA from over 1,200 non-contributors, people who had no contact with any of the mock casework samples, was also employed in the studies. Two and three-person mixtures were made from these samples. FST was used to calculate an LR for each true contributor to each sample. The results showed that not only were they consistent with the qualitative statements but that they were more informative than those statements made prior to using FST.

25. In all, 557,874 comparisons were made between DNA profiles of the non-contributors to the mock samples. When all the calculations and comparisons were finally concluded, they found FST's false positive rate to be very low. Of the more than a half million tests performed, only 163 resulted in a false positive. This meant that FST's overall false positive rate was .03%. Of the false positive results contributing to this rate, the highest number occurred where FST indicated limited support for an inclusion when in reality that person was not a contributor to the mixture. The false positive rate for such instances was .01%. The false positive rate was .0025% where moderate support was erroneously indicated; and a mere .0009% where the erroneous indication was of strong support for an inclusion of a true non-contributor. There was only one instance where very strong support for an inclusion was erroneously indicated.

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[5] Low template samples have extremely low levels of DNA, below 100 picograms (a pictogram is equal to one-trillionth of a gram), while high template samples contain 100 picograms or more of DNA.

26. As part of the validation process, FST was tested using degraded samples. Specifically, 93 mixtures of known contributors were subjected to UV radiation to attempt to replicate degradation found in casework. In addition, studies were done with touched items that replicated casework items that showed various levels of possible degradation. Some of these touched items were also subjected to UV radiation. The results for the touched and purposefully degraded samples demonstrate that the program parameters used were suitable for the type of degraded samples that may possibly be found in casework samples.

27. As part of the validation process, OCME also conducted tests to determine whether the drop-out rates employed by the deducible mode of the program accommodated a range of mixture ratios less extreme than the ratios in the samples from which the drop-out rates were generated. In the executive summary to the validation binders, OCME reported, "To determine whether the drop-out rates employed by the deducible mode of the program accommodate a range of mixture ratios, ratios less extreme than the 5:1:1 and the 4:1 ratios from which the drop-out rates were generated were examined. Of the 439 mixture samples, the following samples were tested for this issue: i. 130 purposeful 3:1:1, 3:1, and 2:1 mixtures[; and] ii. 32 samples of blood punches combined in ratios of 4:1:1 and 2:1:1, 3:1, and 2:1." Exhibit G (Executive Summary) at 3-4. Following the study, the OCME concluded that "[t]he FST program performed well over a wide range of DNA template amounts and mixture ratios and types." Exhibit H (Volume 24A, Summary) at 14.

28. As part of the validation process, the OCME tested whether drop-out at any locus is associated with drop-out at any other loci. See Exhibit I ("Likelihood Ratio

Statistics For Analysis of Single Source, Mixed And Degraded Evidence Samples, Volume 22: Determination of Independence of Drop-Out Among Loci") at 2.

29. Also as part of the approval process, OCME established protocols that are specific to FST and are available on OCME's website. See Exhibit J (Eugene Y. Lien, Technical Leader – Nuclear DNA Operations, "Forensic Biology Protocols for Forensic STR Analysis," dated Feb. 2, 2015, at pages 384-434 ("STR Results Interpretation") and 443-72 ("Forensic Statistical Tool"), available at http://www.nyc.gov/html/ocme/downloads/pdf/Fbio/Protocols%20for%20Forensic%20STR%20Analysis.pdf (last visited February 27, 2015)). Those protocols were reviewed by the Subcommittee as part of the approval process.

30. In total, OCME subsequently presented over 1,000 pages of information to the Subcommittee substantiating its validation study, which comprised 45 binders of data.

31. In October 2010, the Subcommittee voted unanimously to approve the use of FST for forensic casework and issued a binding recommendation to the Forensic Commission. See Exhibit K (Oct. 29, 2010 Letter from DNA Subcommittee). In December 2010, the Commission accepted the recommendation. See Exhibits L (Final Minutes of Dec. 7, 2010 New York State Commission on Forensic Science Meeting) and M (Dec. 16, 2011 letter from New York State Commission on Forensic Science to OCME). As a result, FST is now accredited for use in forensic DNA analysis in New York State.[6]

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[6] Other forensic laboratories employ likelihood ratios to measure probabilities with respect to DNA mixture comparisons. The DNA Subcommittee has separately approved a software program known as TrueAllele, which is now being used by the New York State Police. Other law enforcement bodies use PopStats, a forensic program supplied by the FBI,

32. The protocols developed by OCME for FST testing are reviewed when OCME is audited each year, including audits conducted by outside, independent groups. See Exhibit O (Jan. 4, 2013 Letter from NFSTC to OCME).

33. The OCME has presented FST for peer-review at numerous conferences and in journals. A list of 17 presentations is attached hereto as Exhibit N. The three published articles on FST are attached hereto as Exhibits D, P and Q.

34. The manner in which the DNA in this case was collected from the firearm and the defendant, and the scientific techniques used to isolate and identify the DNA evidence obtained from each are standard and no different from the techniques used in virtually every other case involving DNA in this District. If called at a hearing, an expert from the OCME would testify that swabs taken from locations on the firearm were analyzed per the OCME's standard practice and found to contain the DNA of at least three individuals. Pursuant to a search warrant, DNA was then obtained from the defendant by buccal swab on his inner cheek. The OCME then used a technique known as PCR to copy and amplify the DNA from each sample. Next, the OCME compared the two DNA samples to one another by identifying the number of alleles, which are pieces of DNA, at each of several locations, or "loci." The DNA of every individual contains two sets of alleles at each locus, one from each parent. The number of alleles in each set varies throughout the human population, and thus provides a basis for comparing DNA samples. Again, this is standard practice in the

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which utilizes likelihood ratios to analyze DNA evidence. See John M. Butler, Forensic DNA Typing: Methodology 236 (2011) ("[T]he PopStats estimates include random match probability, combined probability of exclusion/inclusion and likelihood ratios . . . ."). Other software programs, such as LoComatioN, Forensim, LikeLTD, STR Mix, Armed Xpert and LabRetriever have been developed to perform similar analysis.

field of DNA forensics and the defendant does not appear to challenge the use of it in this case under Daubert.

35. Prior to application of OCME's FST software, the results of the comparison of the two sets of DNA could not have been expressed by the CPI because not all of the alleles from Rashawn Smalls's profile were found in the mixture, although he could not be excluded as a possible contributor. In the defendant's case, in one run, 13 of the 15 tested loci on the recovered firearm were found to include sets of alleles matching those of the defendant, along with all or some of the genetic material of two other, unknown possible contributors; in a second run, 11 of the 15 tested loci on the recovered firearm were found to include sets of alleles matching those of the defendant, along with all or some of the genetic material of two other, unknown possible contributors. See Exhibit R (Forensic Statistic Comparison Report, dated Mar. 13, 2014).

36. FST, on the other hand, expresses the probability that the defendant's DNA would be found on the firearm in a different manner. In the defendant's case (where there are at least three potential contributors to the DNA found on the firearm), the software compares (i) the probability that the DNA on the firearm would contain the defendant's DNA plus that of two unknown persons ("Scenario 1"), to (ii) the probability that the DNA on the firearm would contain the DNA of three, unknown persons ("Scenario 2"). Here, FST found Scenario 1 to be 4,190 times more probable than Scenario 2, a ratio that OCME characterizes as "very strong support" for the conclusion that the defendant and two unknown persons contributed to the mixture of DNA found on the firearm rather than three unknown persons. See Exhibit A (June 4 Report).

37. I declare under penalty of perjury that the foregoing is true and correct to the best of my knowledge, information and belief.

Dr. Craig O'Connor

Dated: February 27, 2015
New York, New York